



RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/558,421

DATE: 05/21/2002

TIME: 14:15:59

Input Set : N:\Crf3\RULE60\09558421.raw
Output Set: N:\CRF3\05212002\I558421.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Chatterjee, Deb K.

7 (ii) TITLE OF INVENTION: Mutant DNA Polymerases and Uses Thereof

9 (iii) NUMBER OF SEQUENCES: 43

11 (iv) CORRESPONDENCE ADDRESS:

12 (A) ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.

13 (B) STREET: 1100 New York Avenue, N.W., Suite 600

14 (C) CITY: Washington

15 (D) STATE: DC

16 (E) COUNTRY: USA

17 (F) ZIP: 20005

19 (v) COMPUTER READABLE FORM:

20 (A) MEDIUM TYPE: Floppy disk

21 (B) COMPUTER: IBM PC compatible

22 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

23 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

25 (vi) CURRENT APPLICATION DATA:

26 (A) APPLICATION NUMBER: US/09/558,421

C--> 27 (B) FILING DATE: 26-Apr-2000

28 (C) CLASSIFICATION:

30 (vii) PRIOR APPLICATION DATA:

31 (A) APPLICATION NUMBER: US/08/576,759

32 (B) FILING DATE:

33 (A) APPLICATION NUMBER: US 08/525,057

34 (B) FILING DATE: 08-SEP-1995

35 (A) APPLICATION NUMBER: US 08/537,397

36 (B) FILING DATE: 02-OCT-1995

38 (viii) ATTORNEY/AGENT INFORMATION:

40 (A) NAME: Esmond, Robert W.

42 (B) REGISTRATION NUMBER: 32,893

44 (C) REFERENCE/DOCKET NUMBER: 0942.3600002

46 (ix) TELECOMMUNICATION INFORMATION:

48 (A) TELEPHONE: 202-371-2600

50 (B) TELEFAX: 202-371-2540

53 (2) INFORMATION FOR SEQ ID NO: 1:

55 (i) SEQUENCE CHARACTERISTICS:

56 (A) LENGTH: 40 base pairs

57 (B) TYPE: nucleic acid

58 (C) STRANDEDNESS: both

59 (D) TOPOLOGY: both

61 (ii) MOLECULE TYPE: cDNA

66 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

ENTERED

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Input Set : N:\Crf3\RULE60\09558421.raw
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68 CAGGATCCAC ATGGTGCTTA ACGGCGACAT CCACACTAAG 40
 70 (2) INFORMATION FOR SEQ ID NO: 2:
 72 (i) SEQUENCE CHARACTERISTICS:
 73 (A) LENGTH: 27 base pairs
 74 (B) TYPE: nucleic acid
 75 (C) STRANDEDNESS: both
 76 (D) TOPOLOGY: both
 78 (ii) MOLECULE TYPE: cDNA
 83 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 85 GTTAACTTCT TGTGCGGTCT CAATGAC 27
 87 (2) INFORMATION FOR SEQ ID NO: 3:
 89 (i) SEQUENCE CHARACTERISTICS:
 90 (A) LENGTH: 11 amino acids
 91 (B) TYPE: amino acid
 92 (C) STRANDEDNESS: single
 W--> 93 (D) TOPOLOGY: Not Relevant
 95 (ii) MOLECULE TYPE: protein
 100 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
 102 Ala Lys Ala Ile Thr Phe Gly Ile Leu Tyr Gly
 103 1 5 10
 105 (2) INFORMATION FOR SEQ ID NO: 4:
 107 (i) SEQUENCE CHARACTERISTICS:
 108 (A) LENGTH: 11 amino acids
 109 (B) TYPE: amino acid
 110 (C) STRANDEDNESS: single
 W--> 111 (D) TOPOLOGY: Not Relevant
 113 (ii) MOLECULE TYPE: protein
 118 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
 120 Ala Lys Thr Phe Ile Tyr Gly Phe Leu Tyr Gly
 121 1 5 10
 123 (2) INFORMATION FOR SEQ ID NO: 5:
 125 (i) SEQUENCE CHARACTERISTICS:
 126 (A) LENGTH: 11 amino acids
 127 (B) TYPE: amino acid
 128 (C) STRANDEDNESS: single
 W--> 129 (D) TOPOLOGY: Not Relevant
 131 (ii) MOLECULE TYPE: protein
 136 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
 138 Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly
 139 1 5 10
 141 (2) INFORMATION FOR SEQ ID NO: 6:
 143 (i) SEQUENCE CHARACTERISTICS:
 144 (A) LENGTH: 11 amino acids
 145 (B) TYPE: amino acid
 146 (C) STRANDEDNESS: single
 W--> 147 (D) TOPOLOGY: Not Relevant
 149 (ii) MOLECULE TYPE: protein
 154 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
 156 Ala Lys Ala Ile Asn Phe Gly Leu Ile Tyr Gly

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157      1          5          10
159 (2) INFORMATION FOR SEQ ID NO: 7:
161     (i) SEQUENCE CHARACTERISTICS:
162       (A) LENGTH: 4 amino acids
163       (B) TYPE: amino acid
164       (C) STRANDEDNESS: single
W--> 165       (D) TOPOLOGY: Not Relevant
167     (ii) MOLECULE TYPE: protein
172     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
174     Thr Phe Ile Tyr
175     1
177 (2) INFORMATION FOR SEQ ID NO: 8:
179     (i) SEQUENCE CHARACTERISTICS:
180       (A) LENGTH: 4 amino acids
181       (B) TYPE: amino acid
182       (C) STRANDEDNESS: single
W--> 183       (D) TOPOLOGY: Not Relevant
185     (ii) MOLECULE TYPE: protein
190     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
192     Ala Ile Thr Phe
193     1
195 (2) INFORMATION FOR SEQ ID NO: 9:
197     (i) SEQUENCE CHARACTERISTICS:
198       (A) LENGTH: 4 amino acids
199       (B) TYPE: amino acid
200       (C) STRANDEDNESS: single
W--> 201       (D) TOPOLOGY: Not Relevant
203     (ii) MOLECULE TYPE: peptide
208     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
210     Thr Ile Asn Phe
211     1
213 (2) INFORMATION FOR SEQ ID NO: 10:
215     (i) SEQUENCE CHARACTERISTICS:
216       (A) LENGTH: 45 base pairs
217       (B) TYPE: nucleic acid
218       (C) STRANDEDNESS: both
219       (D) TOPOLOGY: both
221     (ii) MOLECULE TYPE: cDNA
226     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
228 TCAGGCTGCT AAAACATTCA TCTACGGTAT ACTGTATGGT TCTGG          45
230 (2) INFORMATION FOR SEQ ID NO: 11:
232     (i) SEQUENCE CHARACTERISTICS:
233       (A) LENGTH: 33 base pairs
234       (B) TYPE: nucleic acid
235       (C) STRANDEDNESS: both
236       (D) TOPOLOGY: both
238     (ii) MOLECULE TYPE: cDNA
243     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
245 GTAGAGGACC CCGTAATTAA TGGTCTTGGC CGC          33

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325	TAT	TTC	ACA	CTG	TAT	CCA	AAG	GTG	CGA	AGC	TAC	ATC	CAG	CAG	GTT	GTT	334
326	Tyr	Phe	Thr	Leu	Tyr	Pro	Lys	Val	Arg	Ser	Tyr	Ile	Gln	Gln	Val	Val	
327				100					105						110		
329	GCA	GAG	GCA	AAA	GAG	AAG	GGC	TAC	GTC	AGG	ACT	CTC	TTT	GGA	AGA	AAA	382
330	Ala	Glu	Ala	Lys	Glu	Lys	Gly	Tyr	Val	Arg	Thr	Leu	Phe	Gly	Arg	Lys	
331				115					120						125		
333	AGA	GAT	ATT	CCC	CAG	CTC	ATG	GCA	AGG	GAC	AAG	AAC	ACC	CAG	TCC	GAA	430
334	Arg	Asp	Ile	Pro	Gln	Leu	Met	Ala	Arg	Asp	Lys	Asn	Thr	Gln	Ser	Glu	
335				130					135						140		
338	GGC	GAA	AGA	ATC	GCA	ATA	AAC	ACC	CCC	ATT	CAG	GGA	ACT	GCG	GCA	GAT	478
339	Gly	Glu	Arg	Ile	Ala	Ile	Asn	Thr	Pro	Ile	Gln	Gly	Thr	Ala	Ala	Asp	
340				145					150						155		
342	ATA	ATA	AAA	TTG	GCT	ATG	ATA	GAT	ATA	GAC	GAG	GAG	CTG	AGA	AAA	AGA	526
343	Ile	Ile	Lys	Leu	Ala	Met	Ile	Asp	Ile	Asp	Glu	Glu	Leu	Arg	Lys	Arg	
344	160				165					170						175	
346	AAC	ATG	AAA	TCC	AGA	ATG	ATC	ATT	CAG	GTT	CAT	GAC	GAA	CTG	GTC	TTC	574
347	Asn	Met	Lys	Ser	Arg	Met	Ile	Ile	Gln	Val	His	Asp	Glu	Leu	Val	Phe	
348					180					185						190	
350	GAG	GTT	CCC	GAT	GAG	GAA	AAA	GAA	GAA	CTA	GTT	GAT	CTG	GTG	AAG	AAC	622
351	Glu	Val	Pro	Asp	Glu	Glu	Lys	Glu	Glu	Leu	Val	Asp	Leu	Val	Lys	Asn	
352					195					200						205	
354	AAA	ATG	ACA	AAT	GTG	GTG	AAA	CTC	TCT	GTG	CCT	CTT	GAG	GTT	GAC	ATA	670
355	Lys	Met	Thr	Asn	Val	Val	Lys	Leu	Ser	Val	Pro	Leu	Glu	Val	Asp	Ile	
356					210					215						220	
358	AGC	ATC	GGA	AAA	AGC	TGG	TCT	TGA									694
359	Ser	Ile	Gly	Lys	Ser	Trp	Ser										
360				225			230										
363	(2)	INFORMATION FOR SEQ ID NO: 15:															
365	(i)	SEQUENCE CHARACTERISTICS:															
366	(A)	LENGTH: 230 amino acids															
367	(B)	TYPE: amino acid															
368	(D)	TOPOLOGY: linear															
370	(ii)	MOLECULE TYPE: protein															
372	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 15:															
374	Asp	Pro	Asp	Trp	Trp	Ile	Val	Ser	Ala	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	
375	1				5					10					15		
377	Arg	Ile	Leu	Ala	His	Leu	Ser	Gly	Asp	Glu	Asn	Leu	Val	Lys	Ala	Phe	
378					20					25					30		
380	Glu	Glu	Gly	Ile	Asp	Val	His	Thr	Leu	Thr	Ala	Ser	Arg	Ile	Tyr	Asn	
381					35					40					45		
383	Val	Lys	Pro	Glu	Glu	Val	Asn	Glu	Glu	Met	Arg	Arg	Val	Gly	Lys	Met	
384					50					55					60		
386	Val	Asn	Phe	Ser	Ile	Ile	Tyr	Gly	Val	Thr	Pro	Tyr	Gly	Leu	Ser	Val	
387					65					70					75		80
389	Arg	Leu	Gly	Ile	Pro	Val	Lys	Glu	Ala	Glu	Lys	Met	Ile	Ile	Ser	Tyr	
390															85		95
393	Phe	Thr	Leu	Tyr	Pro	Lys	Val	Arg	Ser	Tyr	Ile	Gln	Gln	Val	Val	Ala	
394															100		110
396	Glu	Ala	Lys	Glu	Lys	Gly	Tyr	Val	Arg	Thr	Leu	Phe	Gly	Arg	Lys	Arg	

VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\09558421.raw
Output Set: N:\CRF3\05212002\I558421.raw

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L:27 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:93 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=3
L:111 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=4
L:129 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=5
L:147 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=6
L:165 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=7
L:183 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=8
L:201 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=9
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L:271 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=13
L:460 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=18
L:478 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=19
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L:526 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=21
L:562 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=22
L:580 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=23
L:598 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=24
L:617 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=25
L:635 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=26
L:653 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=27
L:671 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=28
L:689 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=29
L:707 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=30
L:725 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=31
L:742 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=32
L:760 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=33
L:778 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=34
L:805 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=35
L:823 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=36
L:841 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=37
L:862 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=38
L:880 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=39
L:898 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=40
L:916 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=41
L:934 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=42
L:951 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=43